



# Erratum: A candidate gene-based association study of tocopherol content and composition in rapeseed (*Brassica napus*)

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## A commentary on

### A candidate gene-based association study of tocopherol content and composition in rapeseed (*Brassica napus*)

by Fritsche, S., Wang, X., Li, J., Stich, B., Kopisch-Obuch, F. J., Endrigkeit, J., et al. (2012). *Front. Plant Sci.* 3:129. doi: 10.3389/fpls.2012.00129

The publisher regrets that the equation of calculating the percentage of genotypic variation explained by the significant SNPs in the Materials and Methods section was reproduced incorrectly in the above paper.

## CORRECTION

The percentage of genotypic variation explained by the significant SNPs was calculated by  $R_{LR}^2 = 1 - \exp[-\frac{2}{n}(\log L_M - \log L_0)]$  where  $\log L_M$  is the maximum log-likelihood of the model of interest,  $\log L_0$  is the maximum log-likelihood of the intercept-only model,  $n$  is the number of observations (Sun et al., 2010).

## REFERENCES

Sun, G., Zhu, C., Kramer, M. H., Yang, S. S., Song, W., Piepho, H. P., et al. (2010). Variation explained in mixed-model association mapping. *Heredity* 105, 333–340.

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